

February 11, 2021

Health Notice for District of Columbia Health Care Providers
Interim Guidance on SARS-CoV-2 Emerging Variants

SUMMARY

Several significant new variants of SARS-CoV-2 emerged in the fall of 2020 and are circulating globally, including in the United States. On February 11th 2021, the first cases of variant B.1.17 and B.1.351 were detected in the District of Columbia. The emergence of variants has caused widespread concern in the medical and scientific community as well as among the public. Much remains unknown about the SARS-CoV-2 variants. New information about the virologic, epidemiologic, and clinical characteristics of these variants is rapidly emerging. This Health Notice provides information for healthcare providers on what is currently known about the SARS-CoV-2 variants and provides resources providers can use to access the most up-to-date information.

BACKGROUND

Viruses naturally mutate over time. Mutations can have a neutral, negative, or positive effect on viral fitness. Genomic surveillance, our routine analysis of genetic sequence data from test samples, is critical to understand the impact of these mutations, and to understand how variants impact the ability of SARS-CoV-2 to spread more quickly, cause more mild or severe disease, evade detection by commonly used diagnostic tests, and impacts effectiveness of vaccines and therapeutics.

Given that the global COVID-19 pandemic has been going on for more than a year, the emergence of clinically significant new variants is not surprising. There are currently 3 identified variants of particular clinical concern. Once introduced, these variants have the ability to rapidly become the dominant strains in a community or region.

- Variant **B.1.1.7** was first detected in the **United Kingdom** in November 2020.
 - This variant has a large number of mutations (23) most of which are in the spike (S) protein, which the virus uses to attach and enter into human cells.
 - B.1.1.7 is highly transmissible compared to wild-type SARS-CoV-2 and may be associated with an increased risk of death.
 - This variant was first detected in the United States in Colorado in December 2020. It has since been identified in many other states including the District of Columbia.
- Variant **B.1.351** was first detected in **South Africa**.
 - This variant has some of the same S protein mutations found in B.1.1.7.
 - It also appears to be highly transmissible. There is no evidence to date that it is more lethal than wild-type SARS-CoV-2.
 - Preliminary evidence from a non-peer-reviewed preprint article suggests that the Moderna mRNA vaccine may not be as protective against B.1.351 as it is against wild-type SARS-CoV-2¹.
 - Variant B.1.351 was detected in the United States in late January 2021. It has been reported in multiple states including the District of Columbia.
- Variant **P.1** was first identified in Japan in travelers from **Brazil**.
 - P.1 contains 3 mutations in the S protein plus additional mutations that may affect its ability to be recognized by antibodies generated from previous natural infection or through vaccination.
 - A recent study reported on a cluster of cases in Manaus, Brazil². In this region, it is estimated that approximately 75% of the population had been infected with SARS-CoV2 as of October 2020. However, since mid-December the region has observed a surge in cases. The P.1 variant was identified in 42% of the specimens sequenced from late December. The

¹ [biorxiv.org/content/10.1101/2021.01.25.427948v1](https://www.biorxiv.org/content/10.1101/2021.01.25.427948v1)

² [virological.org/t/spike-e484k-mutation-in-the-first-sars-cov-2-reinfection-case-confirmed-in-brazil-2020/584](https://www.virological.org/t/spike-e484k-mutation-in-the-first-sars-cov-2-reinfection-case-confirmed-in-brazil-2020/584)

emergence of this variant raises concerns of a potential increase in transmissibility or propensity for SARS-CoV-2 re-infection of individuals.

- This variant was first detected in the US at the end of January 2021 in Minnesota.

GENOMIC SURVEILLANCE

Beginning in November 2020, the US Centers for Disease Control and Prevention (CDC) has been conducting genomic surveillance to track and better characterize SARS-CoV-2 variants. Through these efforts, genomic data is being made available through public databases for use by public health professionals, researchers, and industry.

Samples from DC residents are being tested via the following programs:

- National SARS-CoV-2 Strain Surveillance (NS3) program
 - The NS3 program collects representative specimen samples on a set schedule from state health departments and other public health agencies for sequencing, evaluation, and further characterization. For more information on the NS3 program see: aphl.org/programs/preparedness/Sequence-Based-Surveillance-Submission
 - The DC Public Health Laboratory (PHL) submits 19 samples every other week, collected from DC hospitals and certain public testing sites.
- Partnerships with commercial diagnostic laboratories to test national samples
- At DC PHL as part of outbreak investigation.

If a variant is identified in DC as part of surveillance testing, DC Health reviews the case data to ensure case investigation and contact tracing were conducted, and to assess for any associated outbreak.

CLINICAL IMPLICATIONS OF SARS-CoV-2 VARIANTS

- More studies are necessary to characterize the effect of the variants on:
 - the clinical presentation of COVID-19 disease
 - the accuracy of COVID-19 diagnostic tests
 - the effectiveness of COVID-19 therapies
 - the effectiveness of COVID-19 vaccines
- The emergence of variants highlights the importance and urgency of widespread vaccination of the population.
- Although variant strains seem to be more transmissible, the mechanism of transmission (e.g., through respiratory droplets between close contacts) is the same.
- As such, infection control and prevention recommendations are unchanged. The importance of following prevention measures such as wearing a mask, practicing social distancing and good hand hygiene, staying home when sick, avoiding crowds, and avoiding poorly ventilated indoor settings should continue to be emphasized to patients.

RESOURCES:

- *Emerging SARS-CoV-2 Variants:* cdc.gov/coronavirus/2019-ncov/more/science-and-research/scientific-brief-emerging-variants
- *Genomic Surveillance for SARS-CoV-2 Variants:* cdc.gov/coronavirus/2019-ncov/cases-updates/variant-surveillance.html
- For updated numbers on variant cases in the United States: cdc.gov/coronavirus/2019-ncov/transmission/variant-cases.html

DC Health will issue additional health alert notices related to the emerging SARS-CoV-2 variants as new information becomes available. For more COVID-19 information visit: coronavirus.dc.gov.

**Please contact DC Health regarding COVID-19 at:
Phone: 202-576-1117 Fax: 202-442-8060 | Email: coronavirus@dc.gov**